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(78)

CLAIMS:

1. An isolated nucleic acid sequence, of an alternative splicing variant of CD40 receptor (CD40R), selected from:

(i) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to SEQ ID NO: 6; or

(ii) nucleic acid sequences having at least 90% identity with any one of the sequences of (i) over the entire length of the sequence.

2. An isolated nucleic acid sequence complementary to the nucleic acid sequence of Claim 1.

3. An amino acid sequence selected from the group consisting of:

(i) an amino acid sequence coded by the isolated nucleic acid sequence of Claim 1; and

(ii) homologues of the amino acid sequences of (i) in which one or more amino acids has been added, deleted, replaced or chemically modified.

4. An amino acid sequence according to Claim 3, as depicted in any one of SEQ ID NO:7 to SEQ ID NO:12.

5. An isolated nucleic acid sequence coding for any one of the amino acid sequences of Claim 3 or 4.

6. A purified antibody which binds specifically to an amino acid sequence present in any of the amino acid sequence of Claim 3 or 4 and not present in native CD40R.

7. An expression vector comprising any one of the nucleic acid sequences of Claim 1 or 5 and control elements for the expression of the nucleic acid sequence in a suitable host.

8. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.

9. A host cell transfected by the expression vector of Claim 7 or 8.

10. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:

(i) the expression vector of Claim 7; and

(ii) any one of the amino acid sequences of Claim 3 or 4.

11. A pharmaceutical composition according to Claim 10, for treatment of diseases which can be ameliorated, cured or prevented by decreasing the level of at least one ligand of CD40R.

12. A pharmaceutical composition according to Claim 10, for treatment of diseases which can be ameliorated, cured or prevented by increasing the level of at least one of the CD40R variants of Claim 1.

13. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:

(i) any one of the nucleic acid sequences of Claim 2;

(ii) the expression vector of Claim 8; and

(iii) the purified antibody of Claim 6.

14. A pharmaceutical composition according to Claim 13, for treatment of diseases which can be ameliorated, cured or prevented by reducing the level of at least one of the CD40R variants of Claim 1.

15. A method for detecting the presence of at least one variant nucleic acid sequence of CD40R in a biological sample, comprising the steps of:

(a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and

(b) detecting said hybridization complex;

wherein the presence of said hybridization complex correlates with the presence of at least one variant nucleic acid sequence in the said biological sample.

16. A method for determining the level of variant nucleic acid sequences of CD40R in a biological sample comprising the steps of:

(a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and

(b) determining the amount of hybridization complexes and normalizing said amount to provide the level of the at least one variant nucleic acid sequences in the sample.

17. A method for determining the ratio between the level of the nucleic acid sequence of a CD40R variant in a first biological sample and the level of the original CD40R sequence from which the variant has been varied by alternative splicing, in a second biological sample comprising:

(a) determining the level of the CD40R variant nucleic acid sequence in the first biological sample according to the method of Claim 16;

(b) determining the level of the CD40R original sequence in the second biological sample; and

(c) comparing the levels obtained in (a) and (b) to give said ratio.

18. A method according to Claim 17, wherein said first and said second biological samples are the same sample.

19. A method according to any of Claims 15 to 18, wherein the nucleic acid material of said biological sample are mRNA transcripts.

20. A method according to Claim 19, where the nucleic acid sequence is present in a nucleic acid chip.

21. A method for identifying candidate compounds capable of binding to the amino acid sequence of Claim 3 or 4 and affecting the binding affinity of said sequences to at least one ligand of CD40, the method comprising:

(i) providing any one of the amino acid sequences as defined in Claim 3 or 4;

(ii) contacting a candidate compound with said amino acid sequence in the presence of at least one ligand of CD40;

(iii) determining the effect of said candidate compound on the binding of said amino acid to said ligand and selecting those compounds which show a significant effect on said binding.

22. A method for detecting any one of the amino acid sequences of Claim 3 or 4 in a biological sample, comprising:

(a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.

23. A method for detecting the level of the amino acid sequence of any one of Claim 3 or 4 in a biological sample, comprising:

(a) contacting with said biological sample the antibody of Claim 6, thereby forming an antibody-antigen complex; and

(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

24. A method for determining the ratio between the level of any one of the amino acid sequences of Claims 3 or 4 of variant CD40R present in a first biological sample and the level of the original CD40R amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

(a) determining the level of the amino acid sequences of Claims 3 or 4 into a first sample by the method of Claim 23;

(b) determining the level of the original CD40R amino acid sequence in the second sample; and

(c) comparing the level obtained in (a) and (b) to give said ratio.

25. A method according to Claim 24, wherein said first and said second biological samples are the same sample.